

Figure 1A

1 GTTGA<sup>.</sup>CTCAT<sup>.</sup>TGCTG<sup>.</sup>TGAA<sup>.</sup>CTTACTGT<sup>.</sup>CAACAGCA<sup>.</sup>CTGTAA<sup>.</sup>CTCATGC<sup>.</sup>CTGAGCCA<sup>.</sup>AAGC 60  
 61 TTGTCTAACACGTATATTTTCTCTGTAAAGCACATCACAGCCTTTCTGCAC<sup>.</sup>TTAGGAACA 120  
 121 TTAGACAGCACTTCAGCAGTACACTTGGGGGCCATTTTAAACAATTAAATCACTGATAGG 180  
 181 CTCCGCTCCGCTCAGGGCGGGCCCCAGACACGGGTTTCCCATGGCAGCACCACGGGCACGCC 240  
 241 CGGCGCACCTGCTGCCCCGAACCCCTGGCTCCAGGGGGCAATGAGGGGGCAGTGGAAGGG 300  
 301 GCACTACTCCTCGGGCATTGCCTAGAGAAGCGAGACCGTCCCGCCCTCCCGCTGGCCCTC 360  
 361 CTTCTCTCCCGCCCGGGGGCCCGCGCAATTCTCCGCCAGAGGGACAGTCGGCCTCATATGT 420  
 1 M L 2  
 421 TAAGACCTCTGATCACTAGATCCCCTGCATCTCCACTGAACAACCAAGGCACCCCTACTC 480  
 3 R P L I T R S P A S P L N N Q G T P T P 22  
 481 CGGCACAAC<sup>.</sup>TCACAAA<sup>.</sup>TCCAATGCGCATGTCCACACTGATGTGGGCAGCCACATGTACA 540  
 23 A Q L T K S N A H V H T D V G S H M Y T 42  
 541 CCAGCAGCCTGGCCACCCTCACCAAATACCCTGTATCCAGAATCAGAAGACTTTGTGATG 600  
 43 S S L A T L T K Y P V S R I R R L C D G 62  
 601 GTACAGAGCCCATAGTTTTGGACAGTCTCAAACAGCACTATTTCACTGACAGAGATGGAC 660  
 63 T E P I V L D S L K Q H Y F T D R D G Q 82  
 661 AGATGTT<sup>.</sup>CAGATATATCTTGAATTTTCTACGAACATCCAAACTCCTCATTCTTGATGATT 720  
 83 M F R Y I L N F L R T S K L L I L D D F 102  
 721 TCAAGGACTACACTTTGTTATATGAAGAGGCAAAATATTTTCAGCTTCAGCCCATGTTGT 780  
 103 K D Y T L L Y E E A K Y F Q L Q P M L L 122  
 781 TGGAGATGGAAGATGGAAGCAGGACAGAGAAACTGGTCGCTTTTCAAGGCCCTGTGAGT 840  
 123 E M E R W K Q D R E T G R F S R P C E C 142  
 841 GCCTTGTTTGTGTGGCCCCAGACCTCAGAGAAAGGATCACGCTAAGTGGTGACAAATCCT 900  
 143 L V C V A P D L R E R I T L S G D K S L 162  
 901 TGGTAGAAGAAGTGTTTCCAGAGATCGGCGATGTGATGTGCAACTTTATCAGTGCAGGCT 960  
 163 V E E V F P E I G D V M C N F I S A G W 182

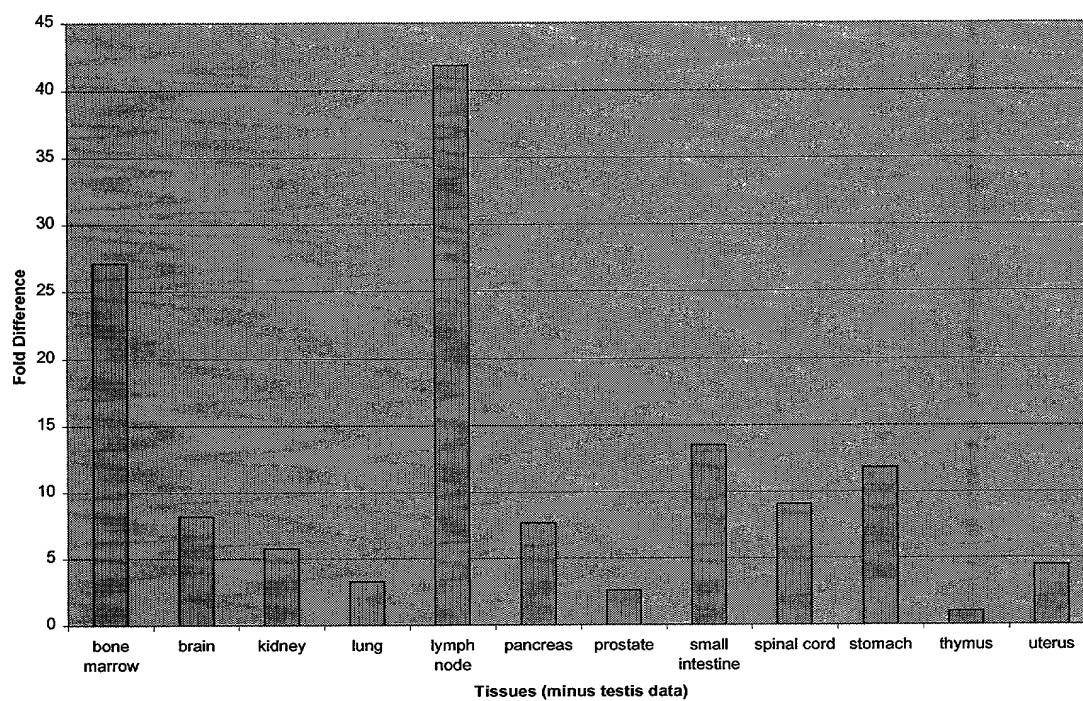
Figure 1B

961	GGAATCATGACTCCACGCACATCGTCAGGTTTCCACTAAGTGGCTACTGTCACCTCAACT	1020
183	N H D S T H I V R F P L S G Y C H L N S	202
1021	CAGTCCAGGTCCTCGAGAGGTTGCAGCAAAGAGGATTTGAAATCGTGGGCTCCTGTAGGG	1080
203	V Q V L E R L Q Q R G F E I V G S C R G	222
1081	GAGGAGTGGGCTCATCCTAGTTCAGCAAATACGTCCTTCATAGGGAAGTGGCGGATGC	1140
223	G V G S S	227
1141	CCTCCCGTACCCTCCATCATCTGGATAAAGCAAGAGCCTCTGGACTAAACGGACATATTT	1200
1201	CTTATGCAAAAAGGAAAAACACACAACTAATAAACAAATAATAAAAAAGGGACATTTGT	1260
1261	GTGCAGTTGGGACAGAAAAACCAAGTCCTGCACCTAAAATTGAATAAAAGATGCATTTATA	1320
1321	TGCAATAGAGACCACACCTGTATTCATATGGGAACAATTGGAATAGTTCACTCAAAAAA	1380
1381	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1418

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Figure 2

		1	50
K+betaM3	(1)	-----	-----
MECHP-2	(1)	-----	-----
KCNMB1	(1)	-----	-----
CG10465	(1)	-----	-----
CG10440	(1)	MDRERERDVKALEPRDLSSSTGRIYARSDIKISSSPTVSPTISNSSSPTPT	
		51	100
K+betaM3	(1)	-----MLRPLITRSPASPINNQ-----	-----GTPTPAQ
MECHP-2	(1)	-----MSRPLITRSPASPINNQ-----	-----GIPTPAQ
KCNMB1	(1)	-----	-----
CG10465	(1)	-----MSTSMGSD-----	-----HKILL
CG10440	(51)	PPASSSVTPGLPGAVAAAGGASSAGASSYLHGNHKPITGIPCVAA	
		101	150
K+betaM3	(25)	LTNSNAHVHTDVGSHMYTSSLATLTQYFVSRIRRLCDGTEPIVLDLSLKQH	
MECHP-2	(25)	LTNSNAPVHTDVGGHMYTSSLATLTQYFVSRIRRLCDGTEPIVLDLSLKQH	
KCNMB1	(1)	-----VVKLVMAQKRCITRALCLGVTMVVCAVITYYILVTVLPLYQ	
CG10465	(14)	KGHSSQYIKLVVGGHLYYITIGTLTKNNDTMSAMESGRMEVITDS-EGW	
CG10440	(101)	ASRYTAPVHTDVGGTMYTSSLETLTQYFESKLAKLFNGQIPIVLDLSLKQH	
		151	200
K+betaM3	(75)	YFTDRDGMFRYLILNFLRTSKLLILDFKDYTLIYEAKYQIQPMLIEM	
MECHP-2	(75)	YFIDRDGMFRYLILNFLRTSKLLIPDFKDYTLIYEAKYQIQPMLIEM	
KCNMB1	(44)	KSVWTQESKCHLEETNIRDDEIKGKVPQYPCLVNVVSAAGRWAFLYHT	
CG10465	(63)	ILIDRCGNHGIILNLRDGTVPPIPTNKELIAELLAEAKYYCITELATSC	
CG10440	(151)	YFIDRDGMFRYLILNFMNRNRIILTADEHPDLELILEARYYEVEPMIKQI	
		201	250
K+betaM3	(125)	ERWKODRETG-----RFSRPCCECLVC-----	
MECHP-2	(125)	ERWKODRETG-----RFSRPCCECLVVR-----	
KCNMB1	(94)	EDTRDONQQC-----S-----	
CG10465	(113)	ERALYAHQEPKPICRIPLITSQ--KEEQLLLSVSLKPAVILVVQRQNNKY	
CG10440	(201)	ESMRKDRVRNGNYLVAPPTPPARHIKTSPTSASPECNYEVVALH-----	
		251	300
K+betaM3	(146)	-----VAPDLRERITLSCDKS-----	-----LVEEVFP
MECHP-2	(147)	-----VAPDLGERITLSCDKS-----	-----LVEEVFP
KCNMB1	(105)	-----YIPGSVDNYQTARADVEK-----	-----VRAKFQ
CG10465	(161)	SYTSTSDDNLLKNIELFDKLSLRNERILFIKDVIGPSEICCWSTYGHGK	
CG10440	(246)	-----ISPDLGERIMLSAARA-----	-----LLDELFP
		301	350
K+betaM3	(169)	EIGDVMCNFIS-AGWNH-----DSTHIVRFPLSGYCHLNSVQVLERLQQ	
MECHP-2	(170)	EIGDVMCNFIS-AGWNH-----DSTHIVRFPLNGYCHLNSVQVLERLQQ	
KCNMB1	(129)	EQQVFYCFSAF---R-GNE-----TSVLFORLYGPQALLFSLFWPTFILT	
CG10465	(211)	KVAEVCCTSVYATDRKHTKVEFPARTIYETLQVLLYENRNAPDQILMQ	
CG10440	(269)	EASQATQSSRSGLSWNQ-----DWQQLIRFPLNGYCKLNSVQVILTRILN	
		351	395
K+betaM3	(212)	RGEIVGSCRGGVGSS-----	-----
MECHP-2	(213)	RGEIVGSCGGVDSSQTFSEYVLRRELRRTPRVPSVIRIKQEPLD	
KCNMB1	(170)	CGHLLIAMVKS-----NOYLSILAAQK-----	-----
CG10465	(261)	ATSSARVGSAGTSSINOYSDEEEERTGLARLRNSNKRNNPS----	
CG10440	(314)	AGETIEASVCG-----QTFSEYILARRVPM-----	

**Figure 3**

**Figure 4.**

<b><u>Protein</u></b>	<b><u>Genbank ID</u></b>	<b><u>Identities</u></b>	<b><u>Similarities</u></b>
Human membrane channel protein-2	gi Y70452	90.7%	92.5%
Human Maxi-K potassium channel beta subunit	gi 4758625	32.0%	32.0%
Drosophila CG10440 protein	gi 7291303	33.1%	42.6%
Drosophila CG10465 protein	gi 17946205	24.0%	38.8%

### Figure 5

